

```

1  GTCTTCACCATGCATCGCTGGGCTTCTTCTCTGTGGGGTGTCTCTCTCTCGCCGGCTG
   +-----+-----+-----+-----+-----+-----+
60  CAGGAAGGTGGTACGTAGCGACCCGGAAGAAGACACCGCACAGAGACGAGCGGGCGAC
   M H S L G F F S V A C S L L A A A -
   +-----+-----+-----+-----+-----+-----+
61  CGCTGTCTCCGGGTCTCGGAGGCGCGCGCGCGCGCGCTTCGAGTCCGGACTCG
   +-----+-----+-----+-----+-----+-----+
   GCACGAGGGCCAGGAGCGCTCCGCGGGCGGGCGCGGAGCTCAGGCCTGAGC
   L L P G P R E A P A A A A A F E S G L D -
   +-----+-----+-----+-----+-----+-----+
121  ACTCTCGGACGCGAGCCCGACCGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG
   +-----+-----+-----+-----+-----+-----+
   TGGAGAGCCTGGCCCTCGGGCTGCGCCGCTCCGGTGCCGAATACGTTTCGTTTCTAGACC
   L S D A E P D A G E A T A Y A S K D L E -
   +-----+-----+-----+-----+-----+-----+
181  AGGAGCAGTTACGGTCTGTCTCAGTGTAGTCAACTCATGACTGTACTCTACCCAGAT
   +-----+-----+-----+-----+-----+-----+
   TCCTCGTCAATGCCAGACACAGGTACATCTACTTGTAGTACTGACATCAGATGGGTCTTA
   E Q L R S V S S V D E L M T V L Y P E Y -
   +-----+-----+-----+-----+-----+-----+
241  ATTGAAAAATGTACAAGTGTACAGTAAAGGAAGGAGGCTGGCAACATAACAGAGAACAGG
   +-----+-----+-----+-----+-----+-----+
   TAACCTTTTACATGTTACAGATCGATTCTCTTCCCTCCGACCGTTGTATGTCTCTTGTC
   W K M Y K C Q L R K G G W Q H N R E Q A -
   +-----+-----+-----+-----+-----+-----+
   CCAACTCAACTCAAGGACAGAGACTATATAAATTTGCTGCAGCACATTATAATACAG

```

MATCH WITH FIG. 1B

FIG 1A

## MATCH WITH FIG. 1A

```

301 -----+-----+-----+-----+-----+-----+-----+
      GGTGGAGTTGAGTTCCTGCTCTCTGATATTTTAAACGAGCTCGTGTAATATTATGTC
        N L N S R T E E T I K F A A A H Y N T E -
                                     +-----+-----+-----+
      AGATCTTGAAAGTATGATTAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361 -----+-----+-----+-----+-----+-----+-----+
      TCTAGAACCTTTTCATPAACTATTACTCACTCTTCTGAGTTACGTACGGTGCCCTCCACA
        I L K S I D N E W R K T Q C M P R E V C -
                                     +-----+-----+-----+
      GTATAGATGTGGGAAGGAGTTTGGAGTCGGACAAACACCTCTTTAAACCTCCATGTG
421 -----+-----+-----+-----+-----+-----+-----+
      CATATCTACACCCCTTCTCAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC
        I D V G K E F G V A T N T F F K P P C V -
                                     +-----+-----+-----+
      TGTCCGCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481 -----+-----+-----+-----+-----+-----+-----+
      ACAGGCAGATGTCTACACCCCAACGAGTTATCACTCCCGAGCTCAGCTACTTGTGTT
        S V Y R C G G C C N S E G L Q C M N T S -
                                     +-----+-----+-----+
      GCACGAGTACCTCAGCAAGAGCTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCA
541 -----+-----+-----+-----+-----+-----+-----+
      CGTGCTCGAGTGGAGTCTGCGAATAAAGTTTAAATGTCACGGAGAGAGATTCCGGGGT
        T S Y L S K T L F E I T V P L S Q G P K -
                                     +-----+-----+-----+
      AACCAGTAACAATCAGTTTGGCCCAATCACACTTCCTGCCGATGCATGCTCTAAACTGGATG
601 -----+-----+-----+-----+-----+-----+-----+
      TTGGTCAATTGTTAGTCAAAACGGTTAGTGTGAAGACGGCTACGTACAGATTTGACCTAC
        P V T I S F A N H T S C R C M S K L D V -

```

MATCH WITH FIG. 1C

FIG. 1B

## MATCH WITH FIG. 1B

```

661  TTTACAGACAAGTTCATTCCATTATAGACGTTCCCTGCCAGCAACTACCACAGTGTC
-----+-----+-----+-----+-----+-----+-----+
AAAATGCTCTGTTCAAGTAAGTAATATCGCAAGGACGGTCGTGTGTGATGGTGTACAG
Y R Q V H S I I R R S L P A T L P Q C Q - 720

AGGCACGGAAACAAGACCTGCCCAACCAATTACATGTGGAATAATCACATCTGCAGATGCC
-----+-----+-----+-----+-----+-----+-----+
TCCGTGCGCTGTTCTGGACGGGTGGTTAAATGATACACCTTATTAGTGTAGACGTCACGG
A A N K T C P T N Y M N N H I C R C L - 780

TGGCTCAGGAAGATTTTATGTTTTTCTCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
-----+-----+-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAATAACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D D S T D G F H - 840

ATGACATCTGTGGACCAACAAGAGAGCTGGATGAAGAGACCTGTGTCAGTGTGCTGCAGAG
-----+-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTGTCTCCTCGACCTACTTCTCTGGACAGTCCACACAGCGTCTC
D I C G P N K E L D E E T C Q C V C R A - 900

CGGGGCTTCGGGCTGCCAGCTGTGGACCCCAAAAGAACTAGACAGAACTCATGCCAGT
-----+-----+-----+-----+-----+-----+-----+
GCCCCGAGCCCGACGTCGACACCTGGGTGTTCTTGTGATCTGTCTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C - 960

GTGTCTGTAAACAACACTCTTCCCCAGCCANTGTGGGGCCCAACCGAGAAATTGATGAAA
-----+-----+-----+-----+-----+-----+-----+
CACAGACATTTTGTGTTGAGAAGGGTCGGTTACACCCCGTTGGCTCTTAACTACTTT
-----+-----+-----+-----+-----+-----+-----+

```

## FIG. 1C

MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

V C K N K L F P S Q C G A N R E F D E N -  
 ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAOCCCTAAATCCTGGAA 1021  
 TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT  
 T C Q C V C K R T C P R N Q P L N P G K - 1080  
 AATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1081  
 TTACACGGACACTTACATGTCTTTTCAGGTGCTTTACGAACAATTTTCTTCTTCAAGG  
 C A C E C T E S P Q K C L L K G K K F H -  
 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCCAGAGGCTTGTGAGC 1141  
 TGGTGGTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACTCG  
 H Q T C S C Y R R P C T N R Q K A C E P - 1200  
 CAGGATTTTCATATAGTGAAGAAGTGTGCTGTGTCCCTTCATATTTGGCAAAGACCAC 1201  
 GTCTTAAAGTATATCACTTCTCACACAGCAACACAGGGAAGTATACCGTTTCTGGTG  
 G F S Y S E E V C R C V P S Y W Q R P Q - 1260  
 AAATGAGCTAAGATTGTACTGTTTCCAGTTTCATCGATTTTCTATTATGGAAACTGTGT

MATCH WITH FIG. 1E

FIG. 1D

## MATCH WITH FIG. 1D

```

1261 -----+-----+-----+-----+-----+-----+-----+
      TTACTCGATTCTTAACATGACAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
      M   S   .
1321 -----+-----+-----+-----+-----+-----+-----+
      TGGCACAGTAGAAGTGTCTGTGAACAGAGAGACCGCTTGTGGGTCCATGCTAACAAAGACA
1381 -----+-----+-----+-----+-----+-----+-----+
      ACGGTGTCATCTTGAACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT
      AAAGTCGTGCTTTTCCCTGAACCATGTGGATAAAGTTTACAGAAATGGACTGGAGCTCATCTG
1381 -----+-----+-----+-----+-----+-----+-----+
      TTTTCAGACAGAAAGGACTTGGGTACACCTATTGAAATGCTTTTACCTGACCTCGAGTAGAC
      CAAAAGGCCCTCTTGTAAAGAETGGTTTTCTGCCAATGACCAAACAGCCCAAGATTTTTCCTC
1441 -----+-----+-----+-----+-----+-----+-----+
      GTTTTCGGGAGAACATTTCTGACCAGAGACGGTTACTGGTTTGTCTGGTTCTTAAAGGAG
      TTGTGATTTCTTTAAAGAATGACTATATAATTTATTTCCACTAAATAATATTGTTTCTCTGC
1501 -----+-----+-----+-----+-----+-----+-----+
      AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTATAACAAAGAGC
      ATTCATTTTATAGCAACAACAATTTGGTAAACTCACTGTGATCAATATTTTATATATCAT
1561 -----+-----+-----+-----+-----+-----+-----+
      TAAGTAAAAAATATCGTTGTTTACCATTTTTGAGTGACACTAGTTATAAAAAATATAGTA
      GCAAAATATGTTTAAATAAAATGAAATTTGTATTTTATAAAAAAATAAAAA
1621 -----+-----+-----+-----+-----+-----+-----+
      CGTTTATACAAAATTTTATTTTACCTTTTAAACATAAATATTTTTTTTTTTTTTT

```

FIG 1E

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```

1  CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGACAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
71  AGATGAACATGACTGTACTCTACCCAGAAATATTGGAATGTACAAGTGTACAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
      M T V L Y P E Y W K M Y K C Q L R
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
-----+-----+-----+-----+-----+-----+-----+
      K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTGCTGCAGCACATTATATACAGAGATCTTGAAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
      I K F A A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTATAGATCTGGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
      R K T Q C M P R E V C I D V G K E F G V
301 CGGCACAAACACCTTCTTTAAACCTCCATGTGTGTCGCTACAGATGTGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
      A T N T F F K P P C V S V Y R C G G C C C

```

FIG. 2A

```

361  CAATAGTCAGGGGCTGCAGTCGATGAACACCAGCAGCTACCTCAGCAAGACGTTATT
      -----+-----+-----+-----+-----+-----+
      N S E G L Q C M N T S T S Y L S K T L F

421  TGAAATTACAGTGCTCTCTCTCAAGGCCCAACACAGTAACAATCAGTTTTCCTCAATCA
      -----+-----+-----+-----+-----+-----+
      E I T V P L S Q G P K P V T I S F A N H

481  CACTTCTCTGCCGATGCATCTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
      -----+-----+-----+-----+-----+-----+
      T S C R C M S K L D V Y R Q V H S I I R

541  ACGTTCCCTGCCAGCAACACTACACAGTGTGAGGCAGCGACAAGACCTGCCCCCAACAA
      -----+-----+-----+-----+-----+-----+
      R S L P A T L P Q C Q A A N K T C P T N

601  TTACATGTGGAATAATCACATCTGCAGATGCTGGCTCAGGAAGATTTATGTTTCCTC
      -----+-----+-----+-----+-----+-----+
      Y M W N N H I C R C L A Q E D F M F S S

661  GGATCTCGAGATGACTCAACAGATGGATTCCATGACATCTGTGACCAACAAGAGCT
      -----+-----+-----+-----+-----+-----+
      D A G D D S T D G F H D I C G P N K E L

```

FIG. 2B

```

721 GGATGAAGAGACCTGTCAGTGTGTCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
    D E E T C Q C V C R A G L R P A S C G P

781 CCACAAAGAAGTAGACAGAACTCATGCCAGTGTCTGTATAAAACAAAACCTCTCCCCAG
    H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTGGGGCCAACCGAGAATTTGATGAAAAACACATGCCAGTGTGTATGTATAAAGAAC
    Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCCTGTGAATGTACAGAAAGTCC
    C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTATAAAGGAAGAAGTCCACCACCAACATGCAGCTGTACAGACG
    Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
    P C T N R Q K A C E P G F S Y S E E V C

```

FIG. 2C



```

1081 TCGTTGTCCTCCCTTCATATTGGCAAGACCACAAATGAGCTAAGATTGTACTGTTTCCA
      -+-----+-----+-----+-----+
      R C V P S Y W Q R P Q M S

1141 GTTCATCGATTTTCTATTATGGAAAAGTGTGTGCCACAGTAGAACTGCTCTGCAACAGA
      -+-----+-----+-----+-----+

1201 GAGACCCCTGTGGGTCCATGCTAACAAAGACAAAAAGTCTGTCTTCTGAAACCATGTGGA
      -+-----+-----+-----+-----+

1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAAGACTGGTTTT
      -+-----+-----+-----+-----+

1321 CTGCCAATGACCAACAGCCCAAGATTTTCCTCTCTGTGATTTCTTTAAAGAAATGACTATA
      -+-----+-----+-----+-----+

1381 TAATTTATTCCACTAAAAATATTGTTTCTGCATTTCATTTTATAGCAACACAATGGT
      -+-----+-----+-----+-----+

1441 AAAACTCACTGTGATCAATATTTTATATATCATGCAAAAATATGTTTAAAAATAAAAATGAAA
      -+-----+-----+-----+-----+

1501 TTGTATTATAAAAAAAAAAAAAAA
      -+-----+-----+-----+-----+

```

FIG. 2D

1 50  
 Pdga .MRTLACLLL LGGYLAVL AEEAIPREV IERARSQIH SIRDQLRLE  
 Pdgb MNRCA.LFL SLCCYLRVLS AEGDPIPEEL YEMLSHSIR SFDDLQRLH  
 Vegf .....MNFLL SWHMSLALL LY ..... LHAKWSOA  
 Vegf2 .....MTV LYPEYKMYK CQ ..... LRKGGWOHN

51 100  
 Pdga IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LP IRRKRSI. ....EEAVP  
 Pdgb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI  
 Vegf APMAE.....GGGQ NHHEVVKFMD .VYOR.....  
 Vegf2 REQANLSRT EETIKFAAH YNTEILKSID NEWRK.....

101 150  
 Pdga AVCKTRTVIY EIPRSQVPT SANFLVPPC VEVKRC TGCC NTSSWKQPS  
 Pdgb AECRTREVF EISRR LIDRT NANFLVPPC VEVORCSGCC NRVVQDRPT  
 Vegf SYCHPIETLV DIFQEPDEI ..EYIFKPC VPLMRGCGCC NDEGLECVPT  
 Vegf2 TQMPREVC I DVGKEFGVAT ..NITFKPPC VSVYRCGCGCC NSEGLQVMT

151 200  
 Pdga RVHRSVKVA KVEYVRKKPK LKEVOVRLEE HLEQAC.....AT.....  
 Pdgb QVQLRPQVR KIEIVRKKPI FKKATVTLED HLAQC.....ETVAARPVT  
 Vegf EESNI TQIM RIK .PH .QG QHIGEMSFQ HNKCECRPK DRARQEKKS  
 Vegf2 STSYLSKTLF EIT.VPLSOG PKPVTISFAN HTSCQMSKL DRYRQVHSII

FIG. 3A

201	Pdgfa	.....TSLNPD YREEDTQVR.	250
	Pdgfb	RSFGSGDEQR AKTPQTRVTI RTVRVRPPK GKHRKFKHTH DKTALKETLG	
	Vegf	RGK.....GKGQKRRK KSRYSWSVY VGARCLMPW SLPGPH.	
	Vegf2	RRSLPATLPQ CQAANKTPT NYMNNHICR CLAQEDFMS SDAGDDSDTG	
251	Pdgfa	.....	300
	Pdgfb	A.....	
	Vegf	CGP.....CSE RRKHLFVQDP QTCKCSKNT	
	Vegf2	FHDTCGNKE LDEETCCVC RAGLRPASCQ PHKEL...DR NSCOCVCKNK	
301	Pdgfa	.....	350
	Pdgfb	.....	
	Vegf	DSRCKARQ LELNERTCRC DKPRR.....	
	Vegf2	LFPSQCCANR EFDENTCCQ VCKRTCPRNQ PLNPGKACE CTESPOKCLL	
351	Pdgfa	.....	398
	Pdgfb	.....	
	Vegf	.....	
	Vegf2	KGKFFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPMIS	

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF $\alpha$	PDGF $\beta$	VEGF	VEGF2
PDGF $\alpha$				
PDGF $\beta$	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

FIG.4

# Expression of VEGF2 mRNA in Human Breast Tumor Cells

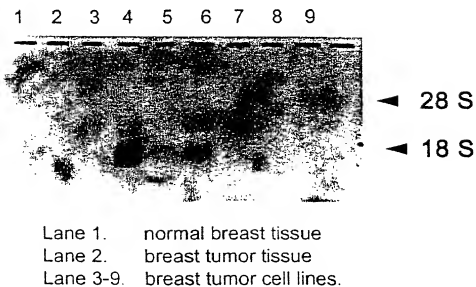


FIG.5

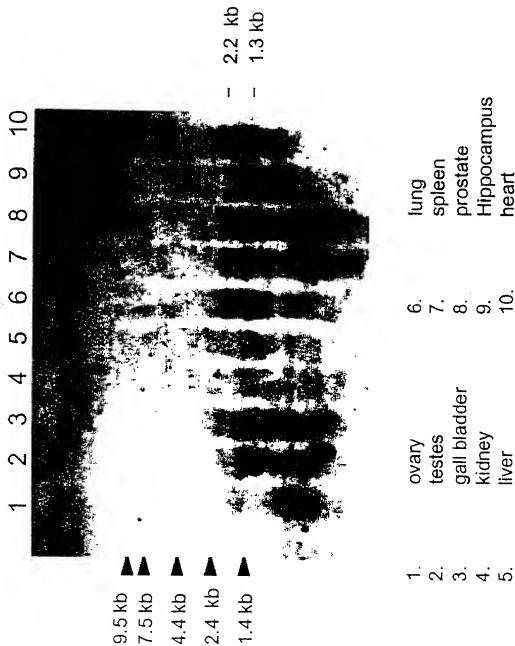
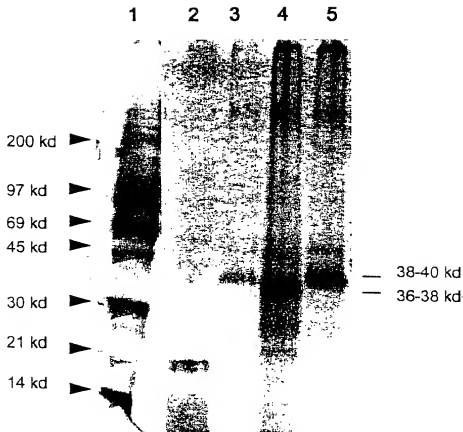


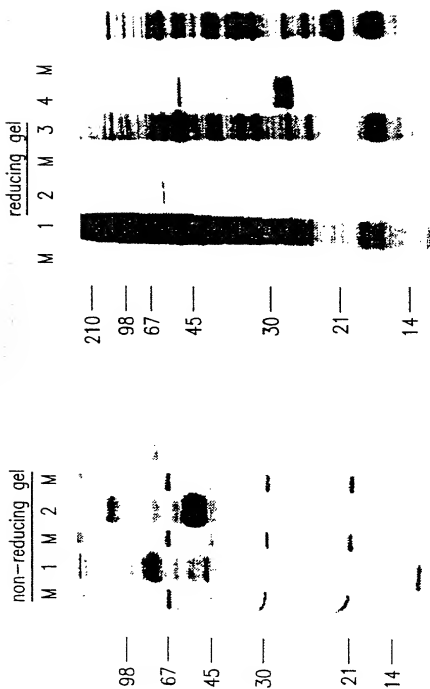
FIG.6

Expression of VEGF2 mRNA in human adult tissues.



- Lane 1: 14-C and rainbow M.W. marker  
 Lane 2: FGF control  
 Lane 3: VEGF2 (M13-reverse & forward primers)  
 Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)  
 Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



Lane M: Marker  
 Lane 1: vector Cytoplasm  
 Lane 2: vector medium  
 Lane 3: VEGF2 Cytoplasm  
 Lane 4: VEGF2 medium

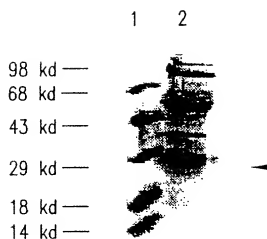
FIG.8B

Lane M: Marker  
 Lane 1: vector medium  
 Lane 2: VEGF2 medium

FIG.8A

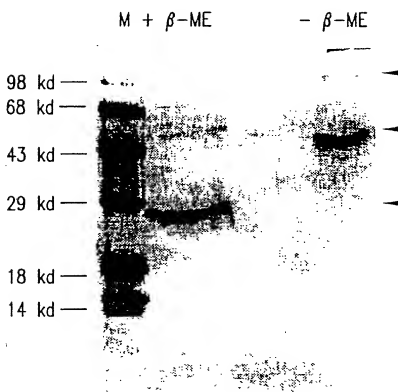


FIG.9



Lane 1: Molecular weight marker  
Lane 2: Precipitates containing VEGF2.

FIG.10



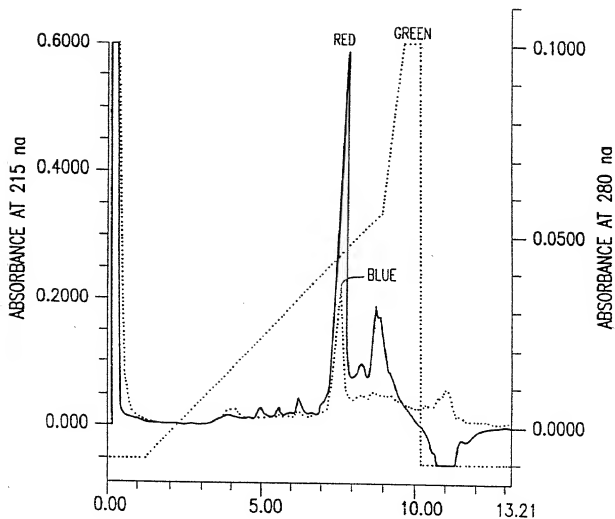


FIG. 11

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FIG.12

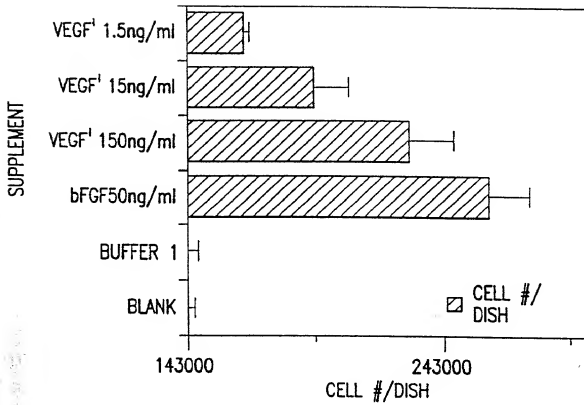


FIG.13

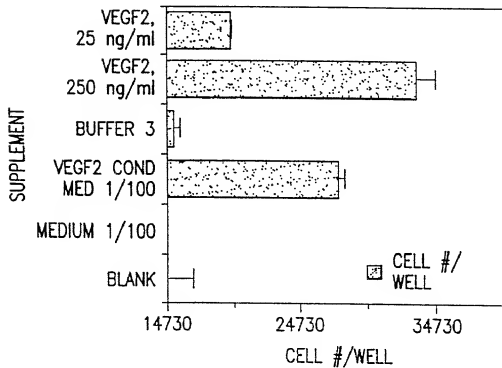


FIG.14A

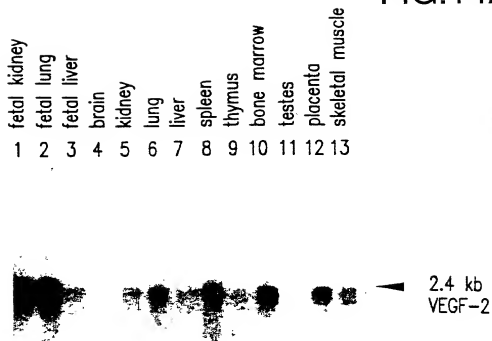
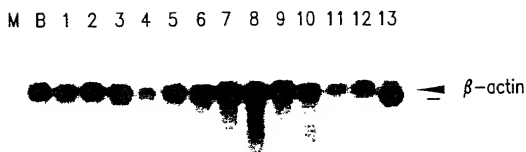
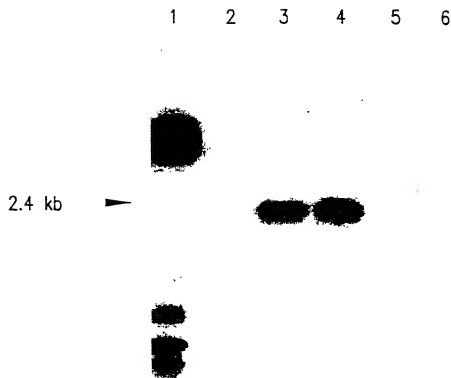


FIG.14B





1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

FIG.15

FIG.16A

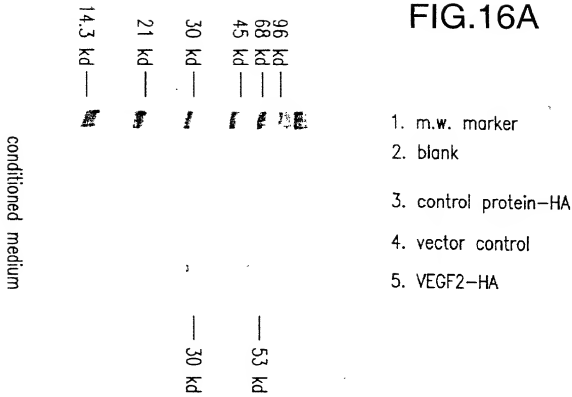
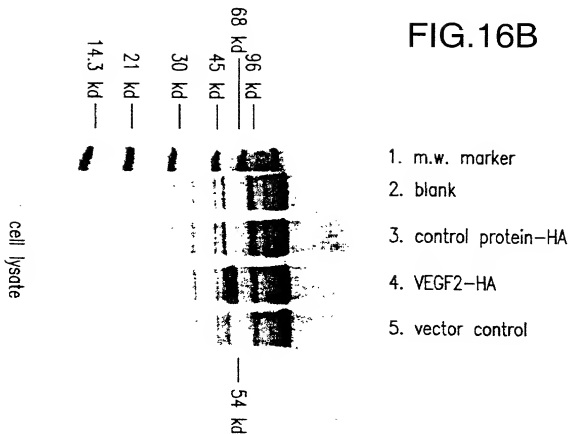


FIG.16B



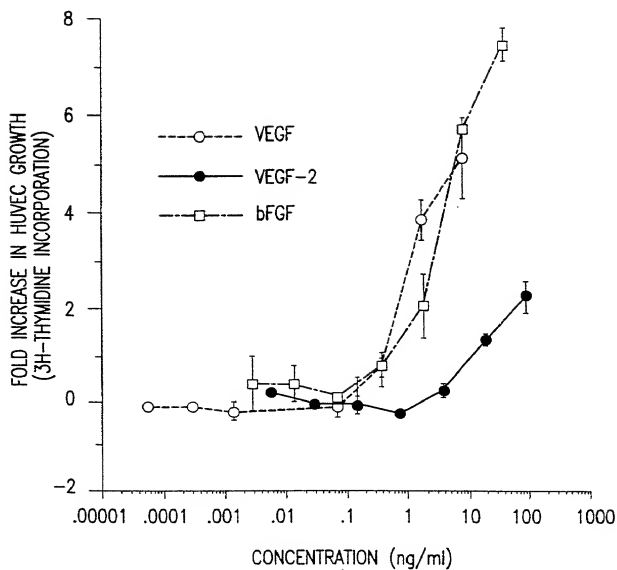


FIG.17

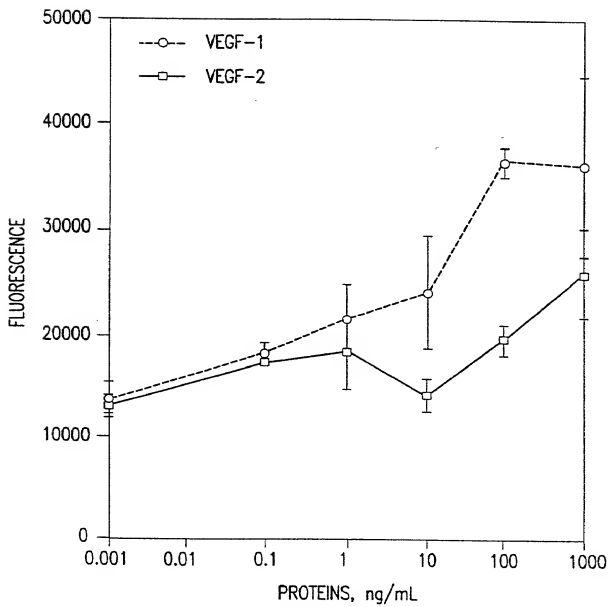


FIG.18



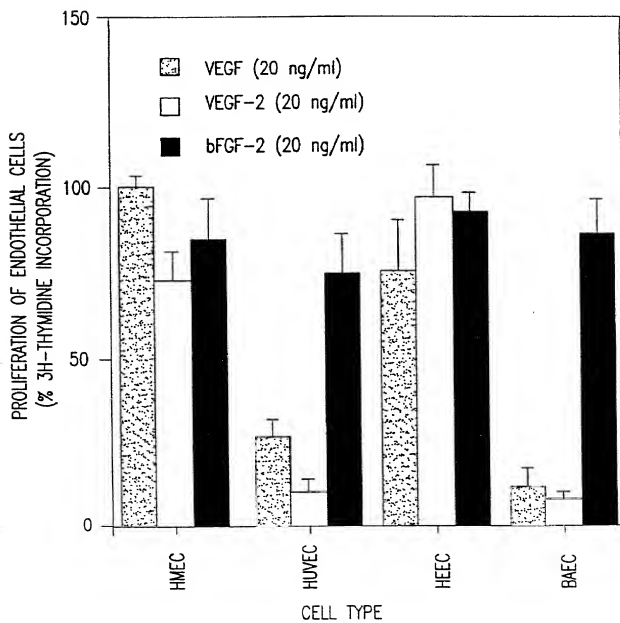


FIG.19

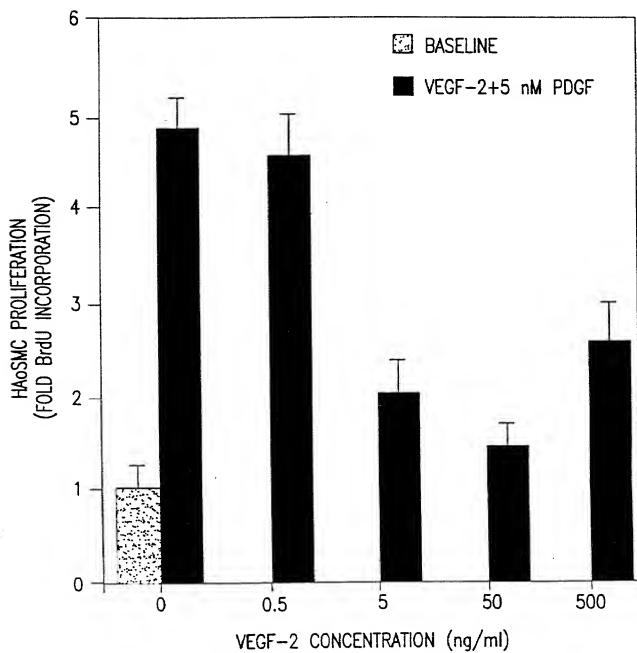


FIG.20A

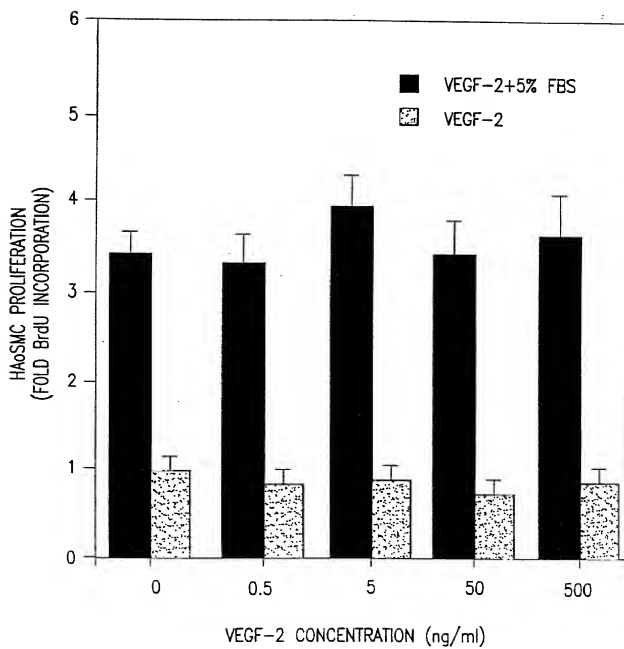


FIG.20B

FIG.21A

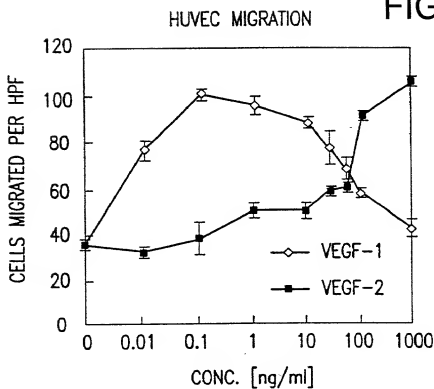
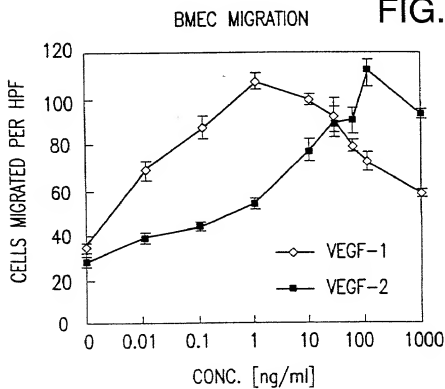


FIG.21B



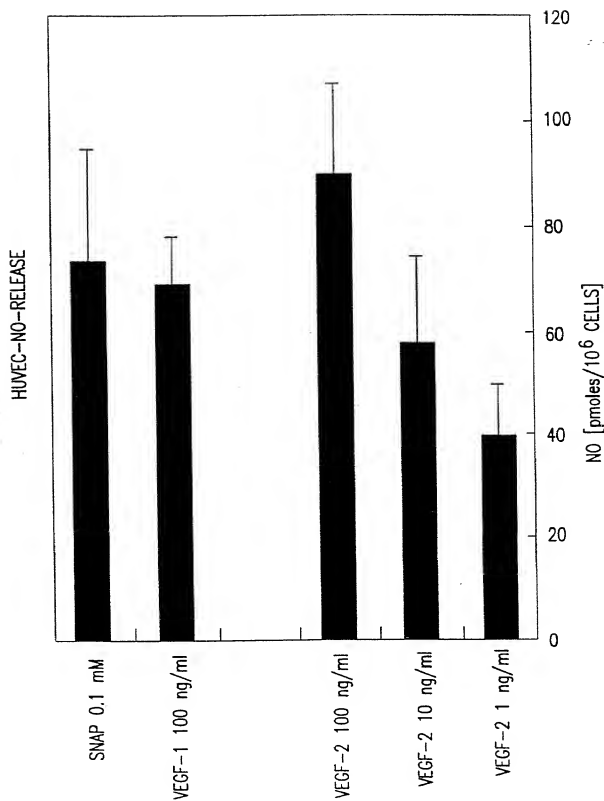


FIG.22

FIG.23

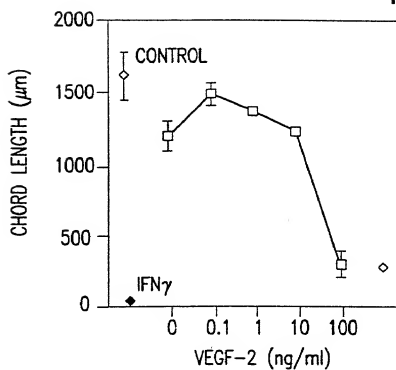


FIG.24

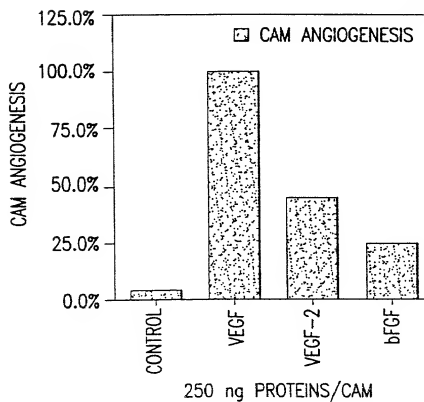


FIG.25A

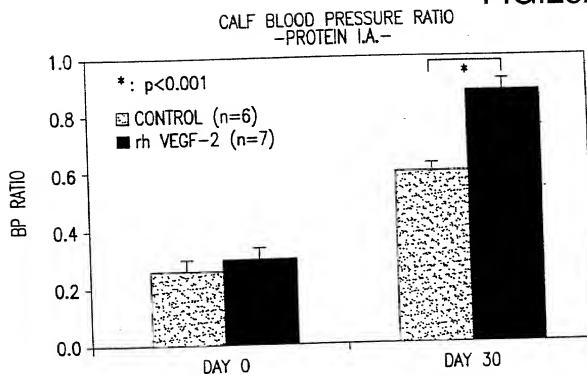
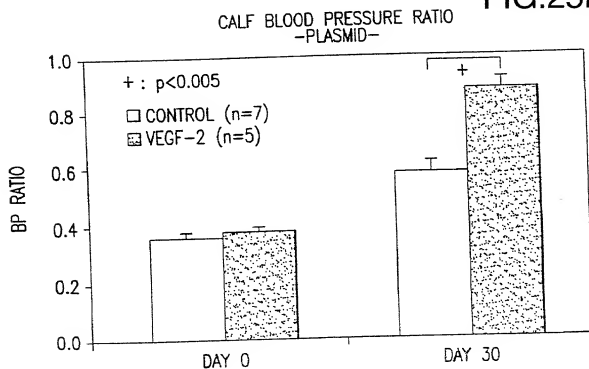


FIG.25B



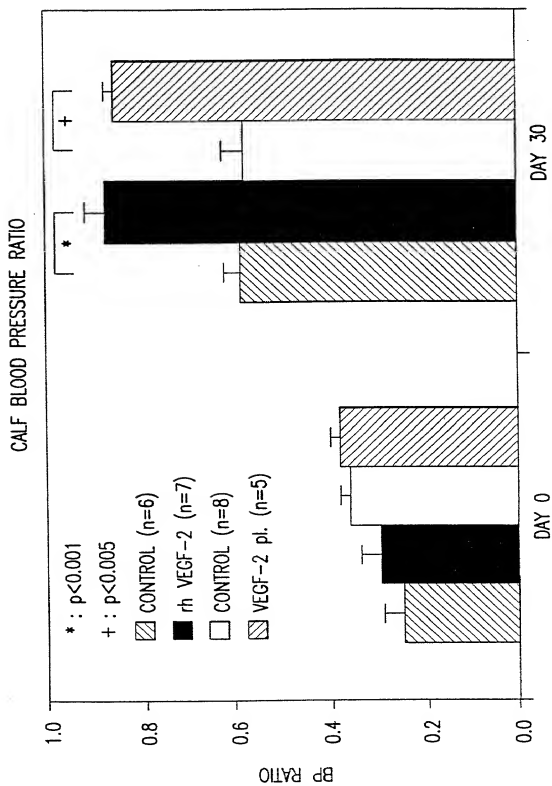


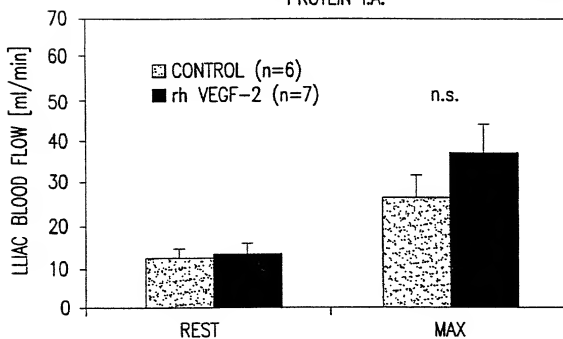
FIG.25C



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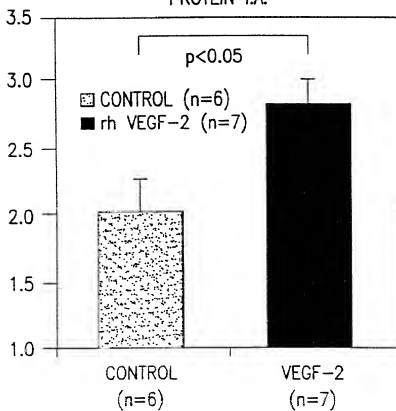
LLIAC BLOOD FLOW  
-PROTEIN I.A.-

FIG.25D



LLIAC FLOW RESERVE  
-PROTEIN I.A.-

FIG.25E



LLIAC BLOOD FLOW  
-PLASMID-

FIG.25F

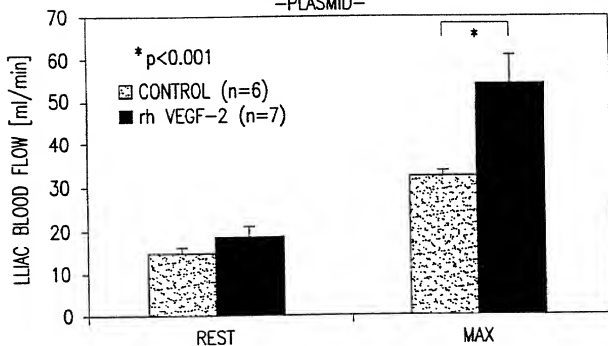
LLIAC FLOW RESERVE  
-PLASMID-

FIG.25G

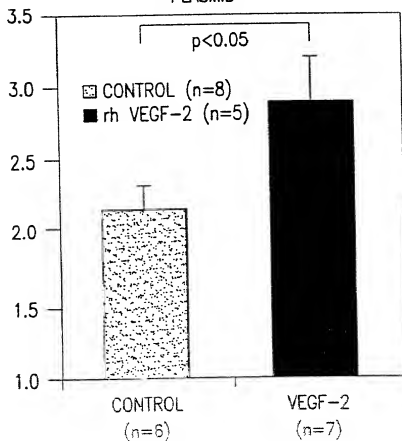


FIG.25H

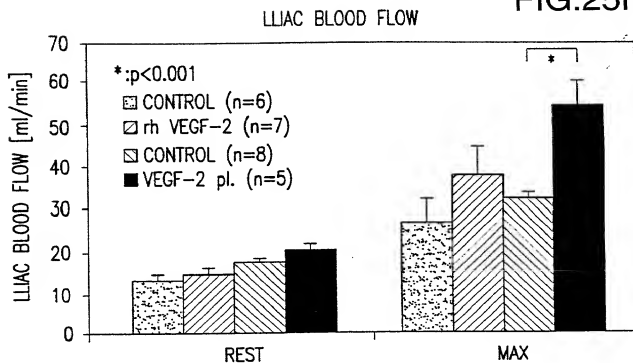
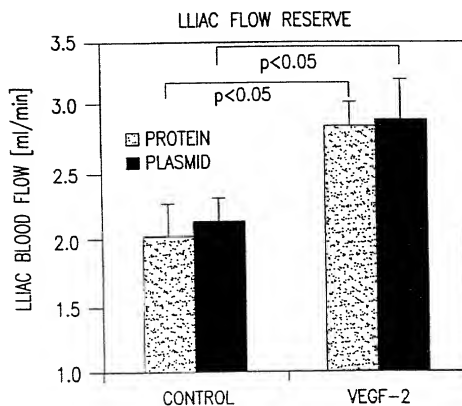
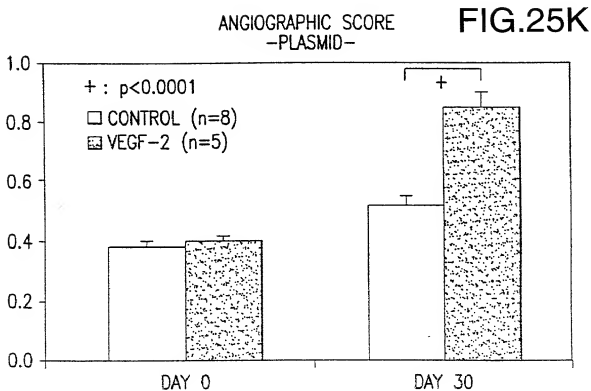
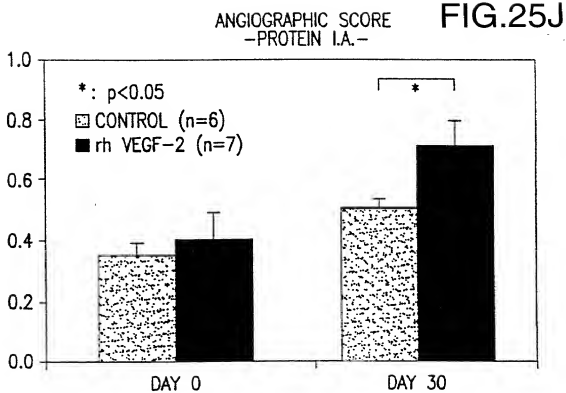


FIG.25I





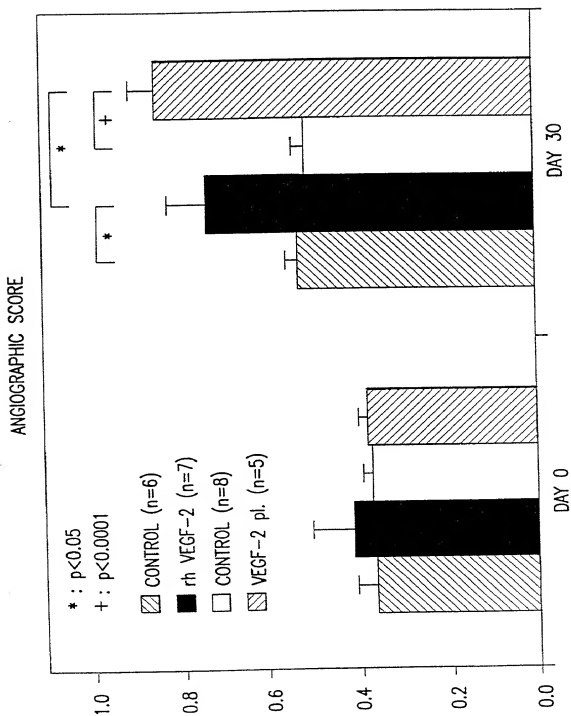


FIG.25L

FIG.25M

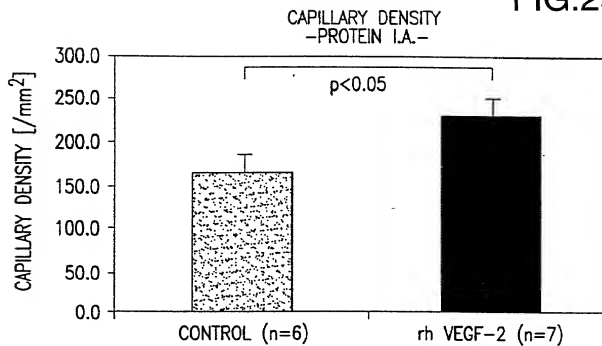
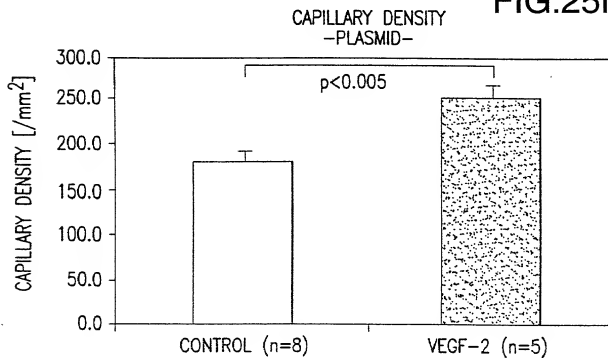


FIG.25N



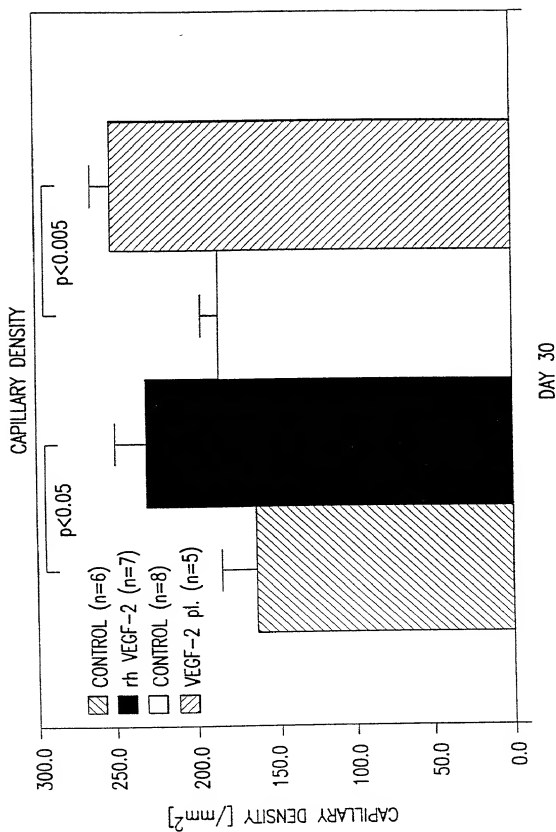


FIG.250

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FIG.26A

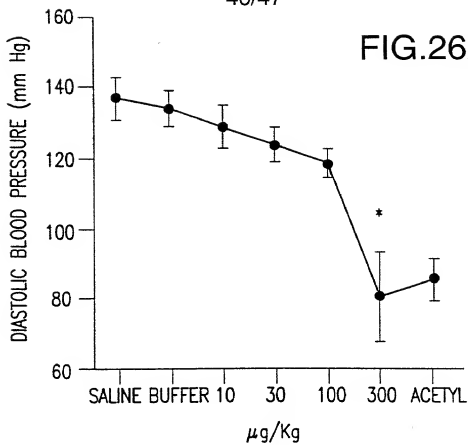
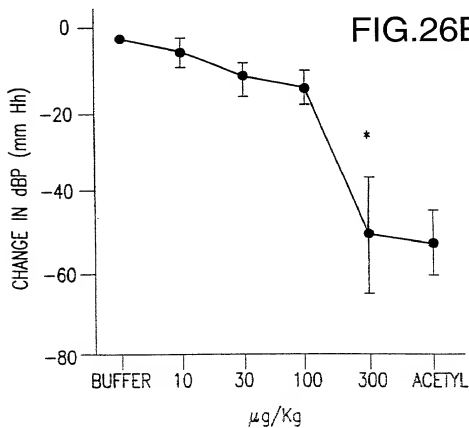


FIG.26B



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FIG.26C

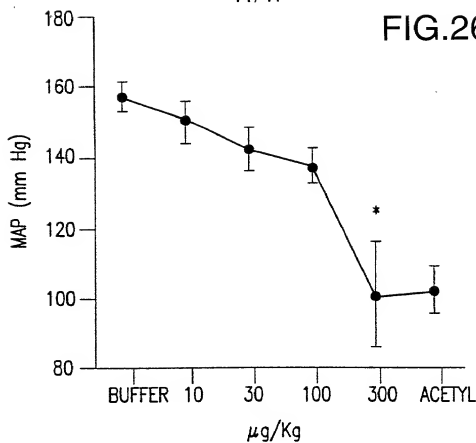
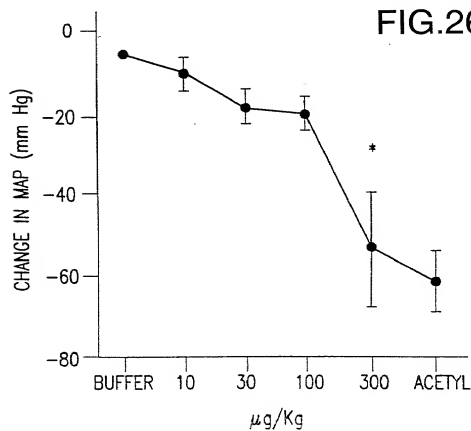


FIG.26D



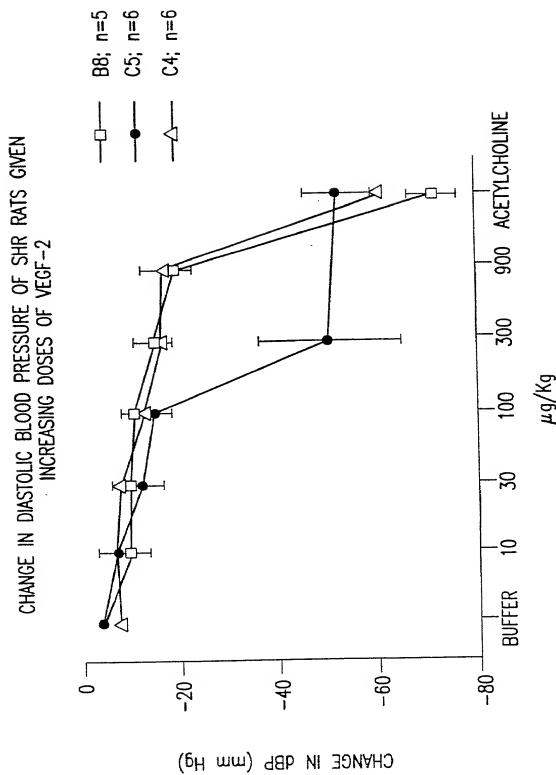


FIG.26E

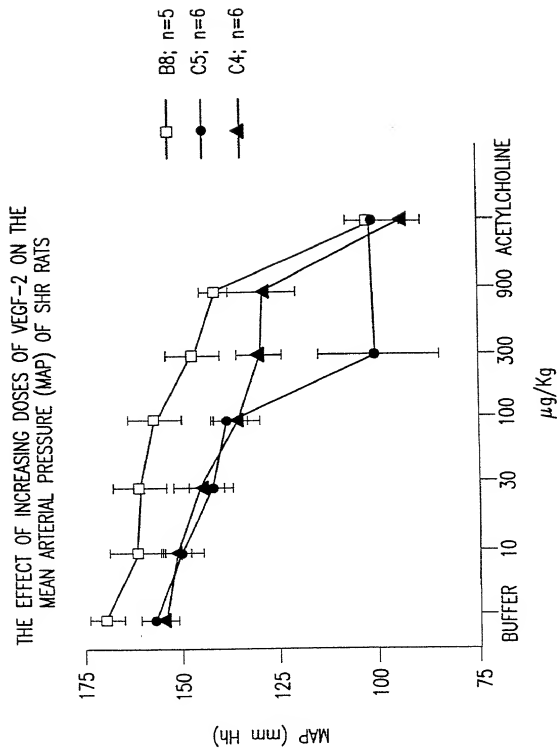


FIG.26F

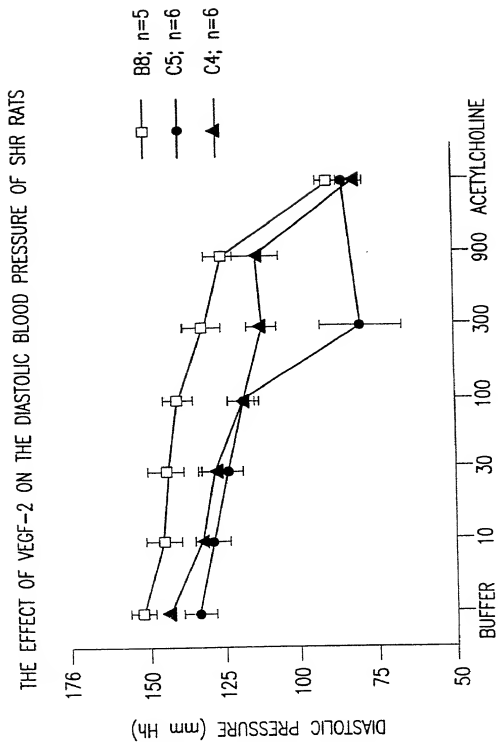


FIG.26G

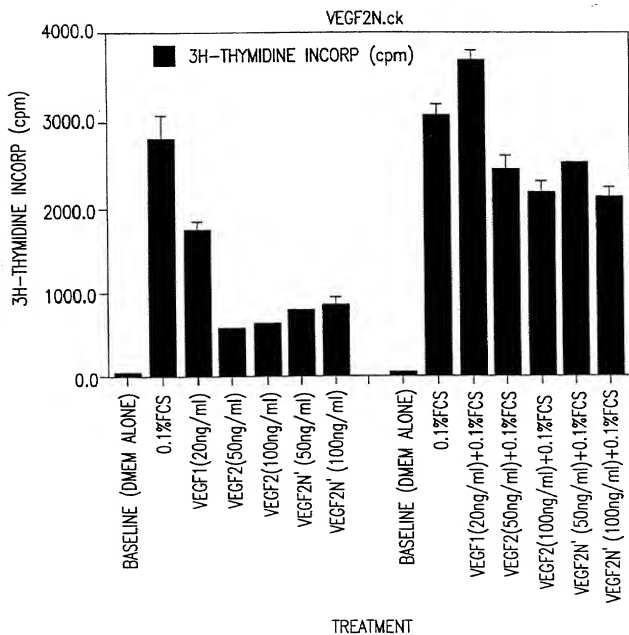


FIG.27

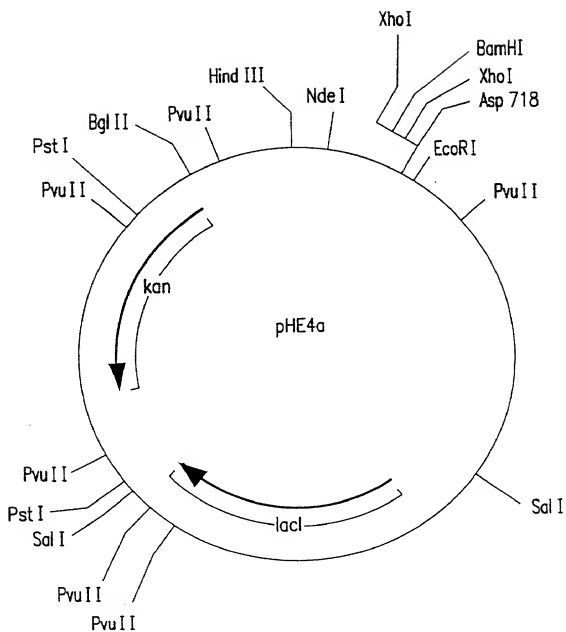


FIG.28

OPERATOR 1

-35

1 AAGCTTAAAACTGCAAAATAGT TTGACT TGTGAGCGGATAAGCAAT

OPERATOR 2

-10

50 TAAGATGTACCCA ATTGTGAGCGGATAACAAT TTCACACATTAA

S/D

94 A GAGGAGAAATTA CATATG

FIG.29